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180886

From: Walicka, Malgorzata
Sent: Tuesday, February 28, 2006 4:42 PM
To: STIC-Biotech/ChemLib

Please search SEQ iD NO:14, 15, 16 and 17 in case 10/763,249.

Thank you.

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Art Unit 1652, Recombinant Enzymes
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400 Dulany St.
Alexandria, VA 22313
Mail Room 2C70
Tel. (571) 272-0944, fax (571) 273-0944

(571)

10/763,249

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 4, 2006, 01:09:25 ; Search time 26.0409 Seconds
(without alignments)
1245.158 Million cell updates/sec

Title: US-10-763-249-15

Sequence: 1.MPNNSQYHTEGAMQTLTP.....LVRAADQMARLLDPLEEA 337

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR 80:*

1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of residues predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1491	81.2	323	2	B83010
2	974.5	53.0	313	2	B82671
3	970.5	52.8	316	2	AC1965
4	957.5	52.1	338	2	AB3453
5	925.5	50.4	320	2	B87401
6	924.5	50.3	329	2	B84515
7	921	50.1	318	2	AD2708
8	921	50.1	318	2	B97490
9	909	49.5	316	2	AC0217
10	901	49.0	317	2	JCS666
11	837.5	45.6	310	2	F81878
12	836.5	45.5	310	2	S39592
13	835.5	45.5	310	2	B81141
14	643	35.0	361	2	B87435
15	593	32.3	323	2	T35734
16	532	29.0	309	2	S73458
17	467.5	25.4	308	2	B64202
18	192	10.5	281	2	S18245
19	188.5	10.3	283	2	T31275
20	184	10.0	286	1	JCS419
21	183.5	10.0	294	2	A59087
22	174	9.5	276	2	JH0245
23	173	9.4	330	2	G87401
24	168.5	9.2	299	2	S68980
25	168.5	9.2	310	2	D90495
26	167	9.1	293	2	T37465
27	166.5	9.1	286	2	G70948
28	165	9.0	266	2	A69358
29	165	9.0	283	2	S10773

30	163	8.9	261	2	T35708	hydrolyase - Strept
31	162.5	8.8	271	2	H97230	alpha/beta superia
32	162	8.8	529	2	T35866	probable secreted
33	161.5	8.8	278	2	S27614	bromide peroxidase
34	161.5	8.8	309	2	D90679	hypothetical prote
35	161.5	8.8	309	2	H85529	hypothetical prote
36	160.5	8.7	309	1	E64762	probable 2,6-dioxo
37	160	8.7	276	2	S76992	probable bromide p
38	160	8.7	231	2	G70605	probable hydrolase
39	158.5	8.6	304	2	E70607	probable hydrolase
40	154	8.4	302	2	AB3196	arylester hydrolas
41	153.5	8.4	356	2	F70636	probable epib prot
42	150	8.2	262	2	E70548	probable bpoc prot
43	150	8.2	283	2	B87546	acetoal dehydrogen
44	149	8.1	266	2	G90785	probable acetyltra
45	149	8.1	266	2	E85645	probable acetyltra

ALIGNMENTS

RESULT 1

B83010

prolyl aminopeptidase PA5080 [imported] - Pseudomonas aeruginosa (strain PA01)

C/Species: Pseudomonas aeruginosa

C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C/Accession: B83010

R/Owner: C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; F

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kae, A.; Lardig, K.; Lim

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path

A/Reference number: A82950; MUID:20437337; PMID:10984043

A/Accession: B83010

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-323 <STO>

A/Cross-references: UNIPROT:Q9HUA3; UNIPARC:UP100000CSEEE; GB:AE004921; GB:AE004091; NI

A/Experimental source: strain PA01

C/Genetics:

A/Gene: PA5080

C/Superfamily: proline aminopeptidase

Query Match	81.2%	Score	1491	DB 2	Length	323			
Best Local Similarity	81.9%	Pred. No.	8.3e-123						
Matches	263	Conservative	32	Mismatches	26	Indels	0	Gaps	0

QY 15 MDTLPQIKPYARDLVAEPHVLVDESSGPEGLPVVFIRHGGAGCDADSRCTFDPNL 74

DB 1 MLVTFEIKPYARHDLVDEPHVLVADSSGPDGLPVFVGGGSGCDALSRFFDPNL 60

QY 75 YRIITFDQGGCRSTPHASLENNNTTWHLVEDLERIREHLDGDKWLVFGSGSTLALAYA 134

DB 61 YRIITFDQGGCRSTPHASLENNNTTWHLVEDLERIREHLDGDKWLVFGSGSTLALAYA 120

QY 135 OTHERRHVGLIKRIFCRPOEIEWYQEGASRLFPDYWDYIAPIPPEERGDVKAFFK 194

DB 121 OTHERRHVGLIKRIFCRPOEIEWYQEGASRLFPDYWDYIAPIPPEERGDVKAFFK 180

QY 195 RLTFNDQIAQMAKAKASTWEGRTATRPNDIVYDRSSEFOALSTARIEHYMNAFL 254

DB 181 RLTFNDQIAQMAKAKASTWEGRTATRPNDIVYDRSSEFOALSTARIEHYMNAFL 240

QY 255 EPDQLRDLPRKIAHLPAVIVHGRYDVICPDNMAALHQAAPNSLKYIRDAHGAASPGI 314

DB 241 RPNQLLEDMRIKIAHLPEVIVHGRYDAICPDNMAALHQAAPNSLKYIRDAHGAASPGI 300

QY 315 TDALVRAADQMARLLDPLEE 335

DB 301 VDALLVRAATIEIGRRLLDPLEE 321

RESULT 2

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 4, 2006, 01:02:32 ; Search time 162.893 Seconds
(without alignment)
1459.714 Million cell updates/sec

Title: US-10-763-249-15

Sequence: 1837
1 MPMNGSQYRTECAMQTLVP.....LVRAADQMARLLDPLEEA 337

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80.*
1: uniprot_sprot.*
2: uniprot_tramb.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1746	95.0	323	2	088D01_PSEPK
2	1601	87.2	323	2	04KIM6_PSEPK
3	1543	84.0	323	2	04Z2H7_PSEPK
4	1530	83.3	323	2	087UX8_PSEPK
5	1491	81.2	323	2	09HUA3_PSEPK
6	1454	79.2	321	2	04IUN2_AZCVI
7	1006.5	54.8	313	2	04UR85_XANCP
8	1006.5	54.8	313	2	08PC98_XANCP
9	1003.5	54.6	313	2	08ENY0_XANCP
10	1001.5	54.5	315	2	07NKP2_GLOVI
11	994	54.1	357	2	04LW33_GLOVI
12	990.5	53.9	315	2	06MHR0_BDEBA
13	988.5	53.8	313	2	05GWM5_XANOR
14	983.5	53.5	313	2	04UR85_XANCP
15	983.5	53.5	321	1	PIP_XYLF
16	979	53.3	312	2	062A61_BURMA
17	976	53.1	312	2	063NU8_BURPS
18	974.5	53.0	313	1	PIP_XYLF
19	971.5	52.9	313	1	PIP_XANCI
20	970.5	52.8	315	2	07WQ23_BOBRP
21	970.5	52.8	316	2	08XIK3_ANNAP
22	965.5	52.6	315	2	07WC24_BOBPA
23	957.5	52.1	316	2	057F44_BRUBA
24	957.5	52.1	316	2	08GK55_BRUBA
25	957.5	52.1	338	2	08YFB4_BRUBA
26	956.5	52.1	315	2	07YB62_BOBPA
27	956	52.0	316	2	092R16_RHIME
28	927	50.5	318	2	0984X4_RHITO
29	925.5	50.4	320	2	09A8X1_CAURA
30	925.5	50.4	322	2	05Y297_NOCRA
31	925.5	50.4	380	2	093Y05_ARATH

32	924.5	50.3	329	1	PIP_ARATH	P93732 arabidopsis
33	922	50.2	317	2	07N3M4_PHOLI	Q7N3M4 photorhabd.
34	921	50.1	318	2	08UG38_AGR75	Q8UG38 agrobacteri
35	916.5	49.9	316	2	05LWK9_SILPO	Q5LWK9 silibacte
36	916.5	49.9	319	2	06ACM6_LEIXX	Q6ACM6 leifsonia x
37	916.5	49.9	329	2	0941B5_ARATH	Q941B5 arabidopsis
38	905	49.5	316	2	08ZFD3_YERPE	Q8ZFD3 yerania pe
39	905	49.3	320	2	08XTB7_RALSO	Q8XTB7 ralsconia s
40	905	49.3	341	2	054KZ1_DICDI	Q54KZ1 dictyosteli
41	902	49.1	316	2	066BV9_YERPS	Q66BV9 yerania ps
42	901	49.0	317	1	PIP_SERMA	Q32449 serricla ma
43	887.5	48.3	351	2	04PHI1_USUMA	Q4PHI1 usuliago ma
44	875.5	47.7	316	2	0607M2_METCA	Q607M2 methylococ
45	869	47.3	319	2	05X473_LEGPA	Q5X473 legionella

ALIGNMENTS

RESULT 1
ID 088D01_PSEPK PRELIMINARY; PRT; 323 AA.
AC 088D01_PSEPK
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Proline iminopeptidase.
GN Name: pip; Ordered locus names: PP5028;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
[1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22423060; PubMed=12534463;
RX DOI=10.1046/j.1462-2920.2002.00366.x;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA Hance I., Chris Lee P., Holtzapfel E.K., Scanlan D., Tran K.,
RA Moralez A., Urtreback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA Wedler H., Lauber J., Stjepandic D., Hohnes J., Streitz M., Helm S.,
RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuenmler B.,
RA Frazer C.M.,
RA *Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";
RL Environ. Microbiol. 4:799-808(2002).
DR EMBL; AB016792; AAN70593.1; -; Genomic_DNA.
DR HSRP; P52279; IACW.
DR MEROPS; S33.001; -.
DR TIGR; PP5028; -.
DR GO; GO:0005737; Cytoplasm; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0016804; F:prolyl aminopeptidase activity; IEA.
DR GO; GO:0019439; P:aromatic compound catabolism; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000073; A/B hydrolase.
DR InterPro; IPR003089; AB hydrolase.
DR InterPro; IPR000639; Epox hydrolase.
DR InterPro; IPR005944; Pept S33.
DR InterPro; IPR002410; Peptidase_S33.
DR InterPro; IPR000379; Ser esters.
DR Pfam; PF00561; Abhydrolase_1; 1.
DR PRINTS; PR00111; ABHYDROLASE.
DR PRINTS; PR00412; EPOXYDRASE.
DR PRINTS; PR00793; PROAMINOPEPTIDASE.
DR TIGR; TIGR01249; pro_1mino_pep_1; 1.
KW Complete proteome.
SQ SEQUENCE 323 AA; 36590 MW; 8044637B6A90BAA CRC64;
Query Match 95.0%; Score 1746; DB 2; Length 323;
Best Local Similarity 99.4%; Pred. No. 5.8e-139;

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Matches 321; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 15 MÖTLYPQIKPYARHDLAVEAPHVLYVDESGSPGGLPVFTHGGAGCDASRCYFPDNL 74
DB 1 MÖTLYPQIKPYARHDLAVEAPHVLYVDESGSPGGLPVFTHGGAGCDASRCYFPDNL 60
QY 75 YRITTFPQRCGRSTPHASLENNNTTWLVEDLERIREHLGIDKVNLFSGSGSTLALAYA 134
DB 61 YRITTFPQRCGRSTPHASLENNNTTWLVEDLERIREHLGIDKVNLFSGSGSTLALAYA 120
QY 135 QTHPERVHGLIRGIFLCRPOEIMFYOGSARLPFDYWDYIAPIPPEERGLVKAFAHK 194
DB 121 QAHHERVHGLIRGIFLCRPOEIMFYOGSARLPFDYWDYIAPIPPEERGLVKAFAHK 180
QY 195 RLITNDQIQAHAAKAWSTWEGRTATLRPNPLVYDRSEEPORALSIARIECHYPMANNAFL 254
DB 181 RLITNDQIQAHAAKAWSTWEGRTATLRPNPLVYDRSEEPORALSIARIECHYPMANNAFL 240
QY 255 EPDQILRDLPKIAHLPVAVHGRYDVICPLDNAMALHQAAMPNSCLKYTRDAGHAASEPGI 314
DB 241 EPDQILRDLPKIAHLPVAVHGRYDVICPLDNAMALHQAAMPNSCLKYTRDAGHAASEPGI 300
QY 315 TDALVRAADQMARRLDLPLEEA 337
DB 301 TDALVRAADQMARRLDLPLEEA 323

RESULT 2
Q4KJMB_PSEFS PRELIMINARY; PRT; 323 AA.
ID Q4KJMB_PSEFS PRELIMINARY; PRT; 323 AA.
AC Q4KJMB_PSEFS PRELIMINARY; PRT; 323 AA.
DT 13-SEP-2005 (Tremblrel. 31, Created)
DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
DE 13-SEP-2005 (Tremblrel. 31, Last annotation update)
DE Proline iminopeptidase (EC 3.4.11.5).
GN Name=PIP; ORFNames=PFL_0411;
OS Pseudomonas fluorescens (strain Pf-5).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=220664;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=PF-5;
RC PubMed=1598061; DOI=10.1038/nbt1110;
RA Paulsen I.T., Press C., Kavel J., Kobayashi D., Myers G.S.,
RA Maurin D., Deboy R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J.,
RA Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosovitz M.,
RA Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Macklin K., Tran K.,
RA Kouri H.M., Pierson E., Pierson L., Thomas L., Loper J.;
RT "Complete genome sequence of the plant commensal Pseudomonas
RT fluorescens Pf-5."
RL Nat. Biotechnol. 23:873-878 (2005).
RM EMBL: CP000076; AAY95820.1; -; Genomic DNA.
KW Aminopeptidase; Hydrolase.
SQ SEQUENCE 323 AA; 36378 MW; DAFAB82442E008A3 CRC64;

Query Match 87.2%; Score 1601; DB 2; Length 323;
Best Local Similarity 91.3%; Pred. No. 1e-126;
Matches 295; Conservative 9; Mismatches 19; Indels 0; Gaps 0;
QY 15 MÖTLYPQIKPYARHDLAVEAPHVLYVDESGSPGGLPVFTHGGAGCDASRCYFPDNL 74
DB 1 MÖTLYPQIKPYARHDLAVEAPHVLYVDESGSPGGLPVFTHGGAGCDASRCYFPDNL 60
QY 75 YRITTFPQRCGRSTPHASLENNNTTWLVEDLERIREHLGIDKVNLFSGSGSTLALAYA 134
DB 61 YRITTFPQRCGRSTPHASLENNNTTWLVEDLERIREHLGIDKVNLFSGSGSTLALAYA 120
QY 135 QTHPERVHGLIRGIFLCRPOEIMFYOGSARLPFDYWDYIAPIPPEERGLVKAFAHK 194
DB 121 QTHPERVHGLIRGIFLCRPOEIMFYOGSARLPFDYWDYIAPIPPEERGLVKAFAHK 180
QY 195 RLITNDQIQAHAAKAWSTWEGRTATLRPNPLVYDRSEEPORALSIARIECHYPMANNAFL 254
DB 181 RLITNDQIQAHAAKAWSTWEGRTATLRPNPLVYDRSEEPORALSIARIECHYPMANNAFL 240

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DB 181 RLITNDQIQAHAAKAWSTWEGRTATLRPNPLVYDRSEEPORALSIARIECHYPMANNAFL 240
QY 255 EPDQILRDLPKIAHLPVAVHGRYDVICPLDNAMALHQAAMPNSCLKYTRDAGHAASEPGI 314
DB 241 EPDQILRDLPKIAHLPVAVHGRYDVICPLDNAMALHQAAMPNSCLKYTRDAGHAASEPGI 300
QY 315 TDALVRAADQMARRLDLPLEEA 337
DB 301 TDALVRAADQMARRLDLPLEEA 323

RESULT 3
Q4ZKH7_PSESY PRELIMINARY; PRT; 323 AA.
ID Q4ZKH7_PSESY PRELIMINARY; PRT; 323 AA.
AC Q4ZKH7_PSESY PRELIMINARY; PRT; 323 AA.
DT 13-SEP-2005 (Tremblrel. 31, Created)
DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
DE 13-SEP-2005 (Tremblrel. 31, Last annotation update)
DE Peptidase S33, proline iminopeptidase 1 (EC 3.4.11.5).
GN ORFNames=Psyr_0375;
OS Pseudomonas syringae pv. syringae B728a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=205918;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=B728a;
RC DOE Joint Genome Institute;
RA Chain P., Larimer F., Dibartolo G., Copeland A., Lykidie A., Trong S.,
RA Nolan M., Goldstein E., Thiel J., Malfatti S., Lapidus A., Detter J.C.,
RA Land M., Richardson P.M., Kyriides N.C., Ivanova N.;
RT "Comparison of two complete genome sequences of Pseudomonas syringae
RT pv. syringae B728a and pv. tomato DC3000."
RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0 (2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B728a;
RA Loper J.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=B728a;
RC Strain=B728a;
RA Feil H., Feil W.S., Lindow S.E.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RM EMBL: CP000075; AAY35445.1; -; Genomic DNA.
GO GO:0016787; F:Hydrolase activity; IEA.
DR GO:0016804; F:prolyl aminopeptidase activity; IEA.
DR InterPro: IPR000073; A/b hydrolase.
DR InterPro: IPR003089; AB_Hydrolase.
DR InterPro: IPR000639; Bbox_Hydrolase.
DR InterPro: IPR005944; Pept_S33.
DR InterPro: IPR002410; Peptidase_S33.
DR InterPro: IPR000379; Ser_estra.
DR Pfam: PF00561; Abhydrolase_1; 1.
DR PRINTS; PR00111; ABHYDROLASE.
DR PRINTS; PR00412; EPOXYHYDROLASE.
DR PRINTS; PR00793; PROAMINOPEPTASE.
DR TIGRFAMs; TIGR01249; pro_imo_1; 1.
KW Aminopeptidase; Hydrolase.
SQ SEQUENCE 323 AA; 36435 MW; 3D1BCC11414EF16 CRC64;

Query Match 84.0%; Score 1543; DB 2; Length 323;
Best Local Similarity 86.4%; Pred. No. 8.1e-122;
Matches 279; Conservative 21; Mismatches 23; Indels 0; Gaps 0;
QY 15 MÖTLYPQIKPYARHDLAVEAPHVLYVDESGSPGGLPVFTHGGAGCDASRCYFPDNL 74
DB 1 MÖTLYPQIKPYARHDLAVEAPHVLYVDESGSPGGLPVFTHGGAGCDASRCYFPDNL 60
QY 75 YRITTFPQRCGRSTPHASLENNNTTWLVEDLERIREHLGIDKVNLFSGSGSTLALAYA 134
DB 61 YRITTFPQRCGRSTPHASLENNNTTWLVEDLERIREHLGIDKVNLFSGSGSTLALAYA 120

```

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 4, 2006, 01:09:25 ; Search time 24.9591 Seconds
(without alignments)
1245.158 Million cell updates/sec

Title: US-10-763-249-17

Perfect score: 1753

Sequence: 1 MQLTYPOIKPVVRHDLAVDE.....LVRAAGDMARLLDLPPEA 323

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum March 0%
Maximum March 100%
Listing first 45 summaries

Database :

1: PIR 80: *
2: p1r1: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1423	81.2	323	2	B83010
2	969.5	55.3	313	2	B82671
3	969.5	55.3	316	2	AC1965
4	938.5	53.5	338	2	AB3453
5	904	51.6	318	2	AD2708
6	904	51.6	318	2	B97490
7	889.5	50.7	320	2	B87401
8	882	50.3	329	2	B84515
9	873	49.8	317	2	UC5696
10	858	48.9	316	2	AC0217
11	830.5	47.4	310	2	S39592
12	823.5	47.0	310	2	F81878
13	821.5	46.9	310	2	B81141
14	625	35.7	361	2	B87435
15	592	33.8	323	2	T35734
16	554	31.6	309	2	S73458
17	483.5	27.6	308	2	B64202
18	199.5	11.4	283	2	T31275
19	196.5	11.2	286	1	UC5419
20	177	10.1	281	2	S18245
21	175	10.0	276	2	JH0245
22	171.5	9.8	283	2	S10773
23	170.5	9.4	294	2	A59087
24	165	9.4	291	2	G70605
25	164.5	9.4	275	2	A71951
26	163	9.3	299	2	S68980
27	162	9.2	266	2	G90785
28	162	9.2	266	2	B85645
29	161.5	9.2	304	2	E70607

30	161.5	9.2	356	2	F70636	probable ephb prot
31	161	9.2	293	2	T37465	probable prolly am
32	159.5	9.1	330	2	G87401	epoxide hydrolase
33	158	9.0	268	2	H69838	chloride peroxidase
34	157.5	9.0	278	2	S27614	bromide peroxidase
35	156	8.9	318	2	H75490	proline iminopeptid
36	152.5	8.7	271	2	B97230	alpha/beta superfa
37	152.5	8.7	275	2	JW0104	azarene carbazole
38	152	8.7	340	2	H98245	lactone-specific e
39	152	8.7	340	2	AD3040	conserved hypothet
40	152	8.7	529	2	T35966	probable secreted
41	151.5	8.6	297	2	T30900	2-hydroxy-6-oxo-6-
42	150.5	8.6	309	2	D90679	hypothetical prote
43	150.5	8.6	309	2	H85529	hypothetical prote
44	150	8.6	266	2	G64842	probable hydrolase
45	149.5	8.5	266	2	A69358	carboxylesterase (

ALIGNMENTS

```
RESULT 1
B83010
prolyl aminopeptidase PA5080 [Imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C:Accession: B83010
R:Stover, C.K.; Pham, X.O.; Eryin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lam,
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: B83010
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-323 <STO>
A:Cross-references: UNIPROT:Q9HUA3; UNIPARC:UPI000000035EE; GB:AE004921; GB:AE004091; NID
A:Experimental source: strain PA01
C:Genetic8:
A:Gene: PA5080
C:Superfamily: proline aminopeptidase

Query Match      81.2% Score 1423; DB 2; Length 323;
Best Local Similarity 78.2% Pred. No. 1.2e-116;
Matches 251; Conservative 33; Mismatches 37; Indels 0; Gaps 0;

OY 1 MQLTYPOIKPVVRHDLAVDEHTTLVDESGSPQGLPVVFTHGPGAGGDANSRCYFENL 60
DB 1 MVLTYPEIKPYARHDLAVDEPHVLYADESGSPDGLPVVFHVGSGGCDALSRFPENL 60

OY 61 YRIYTPORGGGRSTPRASLENNNTWDLVADLERIRHLEIEKVLFGSGWSTLALAYA 120
DB 61 YRIYTPORGGGRSTPRASLENNNTWDLVADLERIRHLEIEKVLFGSGWSTLALAYA 120

OY 121 QTHEDRYLGLIVGIFLARPODIQWFOAGASRLFPDIWQDIYLPAPAEHDMISAYHK 180
DB 121 QTHEDRYLGLIVGIFLARPODIQWFOAGASRLFPDIWQDIYLPAPAEHDMISAYHK 180

OY 121 QTHEDRYLGLIVGIFLARPODIQWFOAGASRLFPDIWQDIYLPAPAEHDMISAYHK 180
DB 121 QTHEDRYLGLIVGIFLARPODIQWFOAGASRLFPDIWQDIYLPAPAEHDMISAYHK 180

OY 181 RLTSNDQIAOMHAKASTWEGRMGLGCPSPOLIERSEPORALSIARIECHYFNNSEFL 240
DB 181 RLTSNDQIAOMHAKASTWEGRMGLGCPSPOLIERSEPORALSIARIECHYFNNSEFL 240

OY 241 EPNGLIDRMKRIATLPGIIVHGRYDMICPLDNAMELHQAAPNSSELQVIREAGHAASEBGI 300
DB 241 EPNGLIDRMKRIATLPGIIVHGRYDMICPLDNAMELHQAAPNSSELQVIREAGHAASEBGI 300

OY 301 TDALVRAAGDMARLLDLPPE 321
DB 301 VDALVRAATNEIGRLDLPPE 321

RESULT 2
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